

Applicants: Christopher C. Fraser (as amended)
Serial No.: 09/766,511 Filed: January 19, 2001
Title: Nucleic acids encoding Tango 405 and functional fragments and uses thereof (as amended)

Atty/Agent: Mario Cloutier Attorney Docket No.: MPI00-537OMNIRCEM

# Replacement Figure Sheet 1 of 39

						•	
	10	20	30	40	50	09	70
Hum.	MRRQPAKVAALLLGLLLECTEAKKHCWYFEGLYPTYYICRSYEDCCGSRCCVRALSIQRLWYFWFLLMMG	LLECTEAKKHO	CWYFEGLYPT	YICRSYEDC	CGSRCCVRAL	SIQRLWYFWE	'LLMMG
,							
Mur.	Mur. MGRKLGRVAALLIGLLVECTEAKKHOWYFEGLYFIYIICKSYEDOOGSROOVKALSIQKEWYFWFLLMMG 10 50 60 70	LVECTEAKKH( 20	CLAXTSEAXMO 30	I I CRAIBDO 40	CGSKCCVKAL 50	SIÇKLWIFWF 60	10 70
	<b>Э</b>	) )		) •	) )	) )	) • .
	80	06	100	110	120	130	140
Hum.	VLFCCGAGFFIRRRMYPPPLIEEPAFNVSYTRQPPNPGPGAQQPGPPYYTDPGGPGMNPVGNSMAMAFQV	YPPPLIEEPA	FNVSYTRQPPI	NPGPGAQQPG	PPYYTDPGGP	GMNPVGNSM	MAFQV
					•••	•••••••••••••••••••••••••••••••••••••••	••
Mur.	VLFCCGAGFFIRRRM	YPPPLIEEPTFNVSYTRQPPNPAPGAQQMGPPYYTDPGGPGMNPVGNTMAMAFQV	FNVSYTRQPPI	NPAPGAQQMG	PPYYTDPGGE	GMNPVGNTM	MAFQV
	80	06	100	110	120	130	140
	ር	ر م	170				
Hum.	Hum. PPNSPQGSVACPPPPAYCNTPPPPYEQVVKAK	AYCNTPPPPYI	EQVVKAK				
			•••••				
Mur.	OPNSPHGGTTYPPPP	SYCNTPPPPYEQVVKDK	EQVVKDK				

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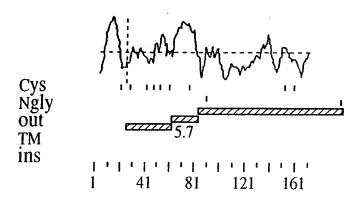


Fig. 1B

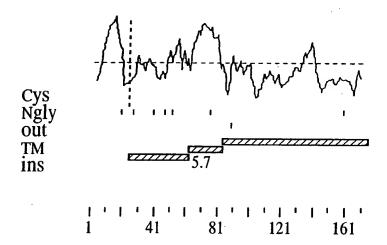
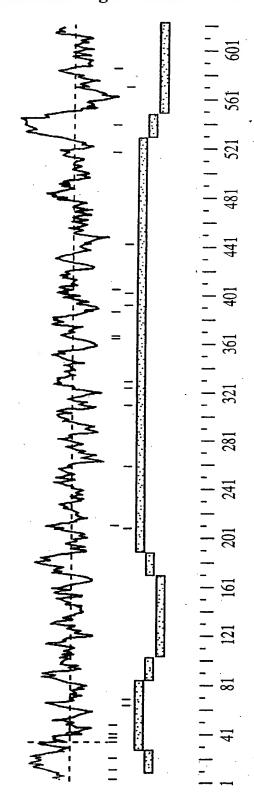


Fig. 1C

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20 30 40 50 60  AILNKVAPQACPAQCS-CSGSTVDCHGLALRSVPRNIPRNTERLDLNG  .:.: .:: ::::::::::::::::::::::::::::	90 100 110 120 130  RVLQLMENKISTIERGAFQDLKELERLRLNRNHLQLFPELLFLGTAKLYRLDL  .: .: .: .: .: .: .: .: .: .: .: .: .: .	200 SFNHMPKLRTF .: TF	270 MAPSCSVLHCP
50 IGLALRSVPRNI .:.: ::::. .NLGLSSIPKNF	120 NHLQLFPELLFLGTA .::: HLYFLFLNNN 110	190 NNNNITRLSVA . : .: : QRNRLTVLGSG'	230 240 250 260 270  DWLRQRPRVGLYTQCMGPSHLRGHNVAEVQKREFVCSGHQSFMAPSCSVLHCP ::VGMVA
40 S-CSGSTVDCH ::: .::	110 IKELERLRLNR : .	180 ALRDLEVLTL .: :.: IDLVSVQYLNL 160	250 JRGHNVAEVQK :: VA
30 VAPQACPAQĆ: :. : -EILGCSSVC: 30	100 STIERGAFQDJ SYVYPKAFVQJ 100	170 SISCIEDGAFI ::: ::: VSFVPRGVFI 150	240 .YTQCMGPSHI 1
20 .AILNK' .TCYLLLLLHK. 20	90 RVLQLMENKI: .: :: 7ALYLDNSNII	160 DIKNLQLDYNÇ : : :::: NLRNLYLQYNÇ	230 WLRQRPRVGLY ::.
10 Slit MRGVGWQMLSLSLGLVL? : : : : : ::.325 MCGLQFSLPCLRLFLVVT	70 80 90 100 Slit NNITRITKTDFAGLRHLRVLQLMENKISTIERGAFQDLKE ::::::::::::::::::::::::::::::::::::	140 150 200 Slit SENQIQAIPRKAFRGAVDIKNLQLDYNQISCIEDGAFRALRDLEVLTLNNNNITRLSVASFNHMPKLRTF: ::::::::::::::::::::::::::::::::::	210 220 Slit RLHSNNLYCDCHLAWLSD 325
Slit 325	Slit 325 <sub>7</sub>	Slit 325	Slit 325

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340 QISELAPDAF	INI	410 DNKLQTIAKG	480 KFRCSAKEQY 	550 NNEFTVLEATGIF .:.: :: SNAFEVLKS
300 340 LTEIPTNLPETITEIRLEQNTIKVIPPGAFSPYKKLRRIDLSNNQISELAPDAF	:: .::::: LRILDLSNNNI 190	350 360 400 410 QGLRSLNSLVLYGNKITELPKSLFEGLFSLQLLLLINANKINCLRVDAFQDLHNLNLLSLYDNKLQTIAKG :: :::::::::::	440 450 460 470 480 FICDCHLKWLADYLHTNPIETSGARCTSPRRLANKRIGQIKSKKFRCSAKEQY ::::YLGSN	510 520 530 540 550 ADLACPEKCRCEGTTVDCSNQKLNKIPEHIPQYTAELRLNNNEFTVLEATGIF .:.:
320 KVIPPGAFSPY		390 KINCLRVDAFQDL ::.: SGFQHL 200	460 SGARCTSPRRL	530 QKLNKIPEHIPQ .:.:.: -NITKVP
310 TEIRLEQNTI		380 SLQLLLLNAN	450 ADYLHTNPIET: :: :: YLGSN	520 GGTTVDCSNQI
300 EIPTNLPETI		370 LPKSLFEGLF	440 ICDCHLKWLAI	510 OLACPEKCRCI
290 IVDCRGKGLT		360 LVLYGNKITE:::	420 430 TFSPLRAIQTMHLAQNPF.	490 500 FIPGTEDYRSKLSGDCFAI
280 Slit AACTCSNNIVDCRGKGI				
Slit	325	Slit 325	Slit 325	Slit 325

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620 SNRITCVGND	NSRIRNVTRD 270	690 VTGNPRCQKP 	760 DVTELYLDGN	ENSD	830 GLKSLRLLSLH :::: -LKPL
560 570 620 620 620 620 600 600 610 620 Slit KKLPQLRKINFSNNKITDIEEGAFEGASGVNEILLTSNRLENVQHKMFKGLESLKTLMLRSNRITCVGND 620 620 620 620 620 620 620 620 620 620	LAN	SFIGLSSVRLLSLYDNQITTVAPGAFDTLHSLSTLNLLANPFNCNCYLAWLGEWLRKKRIVTGNPRCQKP ::::::::: GFSGINNLKHLILSHND	720 730 740 750 760 CDDGNDDNSCSPLSRCPTECTCLDTVVRCSNKGLKVLPKGIPRDVTELYLDGN		ΩΙ
600 RLENVQHKMFK	I	670 LANPFNCNCYLA ::: LEN	740 CLDTVVRCSNK		790 800 810 820 IDLSNNRISTLSNQSFSNM-TQLLTLILSYNRLRCIPPRTF .:.::::::::::::::::::::::::::::::::::
590 GVNEILLTSN:		660 LHSLSTLNLL; : :L]	730 PLSRCPTECTO		800 SNQSFSNM-T( .:.: ::.
580 IEEGAFEGAS( ::.	Ц	65U TTVAPGAFDT]	720 ODGNDDNSCSI	; ; ; ; ; ;	790 DLSNNRISTLS::::::KLDRNRIISII
560 PQLRKINFSNNKITDIEEG :::::	240 240	630 GLSSVRLLSLYDNQIT :: : .:. GINNLKHLILSHND 280	710 2DVAIQDFTCI		780 .SNYKHLTLII :
560 KKLPQLRK:			710 : YFLKEIPIQDVAIQDFT		770 780 OFTLVPKELSNYKHLTL ::: TFSLLKNLIY 300
Slit	) 1	Slit 325	Slit	325	Slit 325

Fig. 2I

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			1
860 870 880 890 900	970 NPCKHGGTCH : .:: -PSMRG	1040 EEKLDFCAQD	1110 EGYSGLFCEF
890 IARCAGPGEMA	930 940 950 960 970  PCLSNPCKNDGTCNSDPVDFYRCTCPYGFKGQDCDVPIHACISNPCKHGGTCH : : : : : : : : : : : : : : : : : : :	1000 1010 1020 1030 1040 EGENCEVNVDDCEDNDCENNSTCVDGINNYTCLCPPEYTGELCEEKLDFCAQD :::NITNCV	1100 TDAVNGYTCICP :: TSSIN
880 IVKSEYKEPG] . : ILAS	950 TCPYGFKGQI	1020 :VDGINNYTCI :V	1090 KCKNGAHCTI :TS
870 CDCNMQWLSDWV :.: :::. CNCKLLGLRDWL	940 NSDPVDFYRC:	1010 DNDCENNSTCV ::: NITNCV 400	1080 DIDFDDCQDN 
860 870 LSHLAIGANPLYCDCNMQWLSDWVKSE : :: .:: ::::: LIHLQANSNPWECNCKLLGLRDWLAS- 360 370	930 SNPCKNDGTC	1000 NCEVNVDDCE	1070 CTPGYVGEHC
850 AFNDLSALSH :::: SSLIH 350	920 NILAKCNPCL :: NI	990 CICADGFEGE: YI	1060 ILTPKGFKCD
840 850 Slit GNDISVVPEGAFNDLSA 325SS	910 920 KFTCQGPVDVNILAKCN : SAITLNI	980 LKEGEEDGFWCICADGF : RALRYI	1050 1060 1070 1080 1090 1100 1110  LNPCQHDSKCILTPKGFKCDCTPGYVGEHCDIDFDDCQDNKCKNGAHCTDAVNGYTCICPEGYSGLFCEF  ::
Slit 325	Slit 325	Slit 325	Slit 325

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	Replacemen	it Figure Sneet	8 of 39
1180 PSAKVRPQTN : :: AWHKV	1250 ELLALDQSLS : :. AVLPVQIQLT O	1320 NSELQDFQKV :.::.	1390 CLPINAFSY :
1120 1130 1180 SPPMVLPRTSPCDNFDCQNGAQCIVRINEPICQCLPGYQGEKCEKLVSVNFINKESYLQIPSAKVRPQTN:.:::::::::::::::::::::::::::::::::	1210 1250 1230 1240 1250 GDKDHIAVELYRGRVRASYDTGSHPASAIYSVETINDGNFHIVELLALDQSLS:::::::::::.	1280 1300 1310 1320 STLNFDSPLYVGGMPGKSNVASLRQAPGQNGTSFHGCIRNLYINSELQDFQKV ::::::::::::::::::::::::::::::::::::	1350 1360 1370 1380 1390 CAHGTCQPSSQAGFTCECQEGWMGPLCDQRTNDPCLGNKCVHGTCLPINAFSY :
1160 GEKCEKLVSV1 : SPI	1230 SHPASAIYSVE' :: PAGRFFQEN	1300 LRQAPGQNGTS	1370 MGPLCDQRTND
1150 EPICQCLPGYÇ	1220 YRGRVRASYDTG : .: FWERIPTS	1290 GGMPGKSNVAS .:.: -SMSGKTSLI- 510	1360 AGFTCECQEGW :
1140 NGAQCIVRIN .:.	200 1210 LYKGDKDHIAVELYR( :	1280 SSTLNFDSPLYV( : ISALPNDAA	1350 AHGTCQPSSQA
1120 MVLPRTSPCDNFDCC :	1200 EDSGILLYK : GSPLEN	1260 1270 128 LSVDGGNPKIITNLSKQSTLNFDSPL :: ::::::::::::::::::::::::::::::::::	1340 EPCHKKV 
1120 - 1120 - Slit SPPMVLPRT - :: 325VSRA	1190 Slit ITLQIATD 325TTN	1260 Slit LSVDGGNF :: 325 TSV	1330 Slit PMQTGILPGC ::: 325 NEAFDILLA- 530

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-	1400	1410	1420	1430	1440	1450	1460
SIIt	SIIT SCKCLEGHGGVLCDEEEDLFNPCQAIKCKHGKCRLSGLGQPYCECSSGYTGDSCDREISCRGERIRDYYQ	/LCDEEEDLE	PCQAIKCKHG	KCRLSGLGQP	YCECSSGYT	3DSCDREIS	CRGERIRDYYQ
	••	•••	•	•	•	•••	•
325	325 AC	VLIII	IIFLIYKVVQFKQKLKA	KLKA	-SNES	1	RENRL-EYY-
	540		550		560		570
	1470	1480	1490	ر 0 م	<u> </u>	ر د تا 1	
Slit	Slit KOQGYAACQTTK-KVSRLECRGGCAGGQCCGPLRSKRRKYSFECTDGSSFVDEVEKVVKCGCTRCVS	TK-KVSRLEC	RGGCAGGQCCG	PLRSKRRKYS	FECTDGSSF	1320 JDEVEKVVK(	GGCTRCVS
	•	•	•••••••••••••••••••••••••••••••••••••••	••	•	••	
325	•	ARYNVTASIC	SFYQSARYNVTASICNTSPNSLESPGLEQIRLHK	LEQIRLHK		QIVPENEAQVI-LFEHSAL	-LFEHSAL
		580	590	009		610	620
				į			
				Fig. 2G			

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70 ATATTATT	140	210 GATGCGC	280 GCACCGC :::
60 CCTTGTTCC	130 TCAGACACI	200 GCGGGGAAA	270 AACAAGGTG
50 SGCTCTACTGO	120 3GCACTGGGCC	160 170 180 190 200 210 3CTAAAGAAAGCCCCCCAGTGCCGGCGGGAAGGTGCGC	260 260 36GCGATCCTG
40 TGCCTGAGTG	110 AGCCCCGCCGC	180 3TGCCGGCGAC	250 3GGTTAGTGCT
30 GGGAGGCGTG			240 CCTGTCGCTG( ::::
20 AGAGGGCGGT	90 CCCTGGCACT	160 CAAGCTAAAG	230 AGATGCTGTC
10 20 40 50 70 Slit CAGAGCAGGGAGGGGGGGGGGGGGGGGGGGGGGGGGGG		150 TCCCTCGGAGCAGCAAC	220 230 240 250 260 270 280 GGCGTTGGCTGCTGTCGCTGGGGTTAGTGCTGGCGATCCTGAACAAGGTGGCACCGC :::
Slit	325 Slit	325 Slit	

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350 350 3:: 3::	420 .acgaag	490 .ccattgaaa ::::: ccttta	560 CTGTTTCC ::::
340  GGCGCTGCC	410 ACAAGAATI	480 TTAGCACCP ::-	550 CCTTCAGCT
330 CTGTCACGGGCT :::: CACG	400 3GAAATAACATC	440 450 460 470 480 490  TTAGACATCTAAGAGTTCTTCAGCTTATGGAGAATAAGATTAGCACCATTGAAA ::::::::::::::::::::::::::::::::	540 TTAAACAGAAATCAC ::::: :: TTAATAATACG- 80
320 GCACAGTGGA(	390 GGATTTAAATC	460 470 GTTCTTCAGCTTATGGAGAATAA ::::::::::::::::::::::::::	530 SACTGCGTTTA ::: 5TTA
310 TGCTCGGGCA	380 ACCGAGAGACT	450 TCTAAGAGTT( :::	520 GAACTAGAGAGA : : : : : : - : - AGCT-GAGTG-
300 GCAGTGCTC1	370 cccccaaaca	440 STCTTAGACA	510 CCAGGATCTTAAA :.:::: -CTGAATC
290 340 350 350 350 350 340 350 340 350 340 350 340 350 340 350 340 350 340 350 340 350 340 350 340 350 340 350 350 340 350 350 340 350 350 340 350 350 340 350 350 350 350 350 350 350 350 350 35	360 370 380 420 GCCCAGGAATATCCCCCCCCAACACCGAGAGACTGGATTTAAATGGAAATAACATCACAAGAATTACGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGA	430 Slit ACAGATTTTGCTGGTC	500 510 520 530 540 550 560 GAGGAGCATTCCAGGATCTTAAAGAACTAGAGACTGCGTTTAAACAGAAATCACCTTCAGCTGTTTCC ::::::::::::::::::::::::::::::
Slit 325	Slit 325	Slit 325	slit 325

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	_	*	
630 GCAATC :	700 GCTGTA ::: GTT	770 TACTAG	840 CTGTAT :: AT
620 AAAACCAAATTCAG ::::::::::::::::::::::::::::::::::::	690 AACCAGATCA	760 NTAACAACAT N	830 TCAAACAAC
580 620 630 630 GGGACTGCGAAGCTATACAGGCTTGATCTCAGTGAAAACCAAATTCAGGCAATC : ::.:::::::::::::::::::::::::::::::::	680 AACTGGATTACAA ::::::: TGGATTACA- 140	750 CACTCTCAACAAT :.:::: CTACGA- 170.	820 FTTCGACTGCAT ::: FTT
600 CAGGCTTGAT	670 AAAAATTTGC; .:.::: -GATATGTG	740 'GGAAGTGCT( ::: 'TGC	810 CTTAGGACTTTT .::::
590 6 CTGCGAAGCTATACAGGC : :::::::: CCAATTCTGATCTGA 100 110	660 AGTTGACATAA	730 CTCCGGGACCT( :: .:: CTGCCT·	800 CATATGCCTAAA :. :: CTGTTA
580 TTGGGACTG:::	650 CCGTGGGGC	720 TTCAGGGCTCT :::: CTCT	780 790 8 CTGTGGCAAGTTTCAACCATATG :::: ::: .::: .:: CTGTTTCTGGTTGTTACCTGTTA
570 Slit TGAGTTGCTGTTTCTTG : :::::: 325 TTTTCTTG	640 650 670 670 680 690 700 CCAAGGAAAACTTTGCAACTGGATTACAACCAGATCAGCTGTA 6.:.::::::::::::::::::::::::::::::::::	710 720 730 740 750 760 770 770 770 770 770 770 770 770 77	780 800 810 820 840 ACTITCTGTGGCAAGTTTCAACCATATGCCTAAACTTAGGACTTTTCGACTGCATTCAAACAACTGTAT ::::::::::::::::::::::::::::::::::
Slit 325	Slit 325	Slit 325	Slit 325

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910 CTCAGT :: :	980 TCTGCAGTGG ::::::: TCTGCACTGG 250	1050 AACAAT	1120 AATAC :.:
900 STTGGTCTGTACACT :::::::::::::::::::::::::::::::::	970 3AGAATTTGTCTGCA :::::: TCTGCA	1040 TGTACCTGTAGCA::: -GTAACTTAGGC-	1070 1080 1090 1100 1110 1120 1120 1120 1120 112
890 GGCCTCGGC :: TAC	960 ICAAAAACG	1030 CCTGCCGCC	1100 ATCTTCCAGAGA :: :::::: ATTTTCCTGAAA 310
880 TTCGCCAAAGGC :::::: AAATAC 220	950 'AGCCGAGGT' ::: AGC	1020 TTGCACTGCC ::::::	1090 TCCCCACAAA
870 STCCGACTGGC	940 3GCCATAATGT	1010 TTGTAGTGTT	1080 'CTCACTGAGA' : :::: 'CCTAAGA'
860 GGCCTGGCTC .: AG	930 CACCTGAGAG	1000 TGGCTCCTTC	1070 TGGGAAAGGTCT :: .: :: AGTATTC-
850 860 870 880 890 900 910  Slit TGTGACTGCCTGGCTCTCCGACTGGCTTCGCCAAAGGCCTCGGGTTGGTCTGTACACTCAGT ::::::::::::::::::::::::::::::::::::	920 930 940 950 960 970 980 GTATGGGCCCTCCCACCTGAGGGCCATAATGTAGCCGAGGTTCAAAAACGAGAATTTGTCTGCAGTGG :::: :: :: :: :: :: :: :: :: :: :: :: :	990 1000 1010 1020 1030 1040 1050  TCACCAGTCATTTATGGCTCCTTGTAGTGTTTTGCACTGCCCTGCCGCCTGTACCTGTAGCAACAAT ::::::::::::::::::::::::::::::::	1060 ATCGTAGACTGTCGTG :::::: CTTTCGAG
Slit 325	Slit 325	Slit 325	Slit 325

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	_	3	,
1190 TTAGACGAAT :. ::: AAAGT-GAAT 370	1260 GAATTCA ::::	1330 CTTACAGC :::::: CTAACA	1400 ACAACTTGAA ::.::.:. -CATCTATAT 460
70 CATATAAAAAGCTTA :.:::::::: CTTATATAAATGAAA 360	1250 ACGCTCTCT .: TC	1320 13 CTGTTTTCCTTACA :: :::: TAATTCTAACA	1390 ATCTCCACA::.
1160 1170 1180 1190  CTGGAGCTTTCTCACCATATAAAAAGCTTAGACGAAT ::::::::::::::::::::::::::::::::::	1240 TTCCAAGGACTAC ::::::::::::::::::::::::::::::::::	0 AGTTTATTTGAAGGA:::::::: ATTGTATTTGGA	1380 .TGCTTTTCAGGA : :.:: TTCAATTGAGG- 450
1160 CCTGGAGCTTT ::::. : CTGGGAATAA 340	1230 ?ACCAGATGCT	1300 CCCAAAAGTT : : ATTG	1370 GCCTTCGGGTAGA :::::: GCCTTTG
1150 AGTCATCCCTC	1220 CTGAACTTGC	1290 CACAGAACTC :::	1360 ATAAACTGCC ::: GCC
1140 CACAATCAAA	1210 AATCAGATC1 	1280 GAAATAAAAT	1350 IGCCAACAAG: :::::: I-CCAAAA
1130 1140 1150 1160 1170 1180 1190  Slit GTTTGGAACACAATCAAAGTCATCCCTCCTGGAGCTTTCTCACCATATAAAAAGCTTAGACGAAT ::::::: 325TGTATCTGA	1200 1250 1260  TGACCTGAGCATAATCAGATCTCTGAACTTGCACCAGATGCTTTCCAAGGACTACGCTCTCTGAATTCA :::: TAACAGGACTTCATTCT	1270 1280 1300 1310 1330 Slit CTTGTCCTCTATGGAAATCACAGAACTCCCCCAAAAGTTTATTTGAAGGACTGTTTTCCTTACAGC ::::: 325 CTTGTTAATTCTAAAATCACAGAACTCCCCAAAAGTTTTTGGACTGTTTTTTACTTAACACACAC	1340 1350 1360 1370 1380 1400 Slit TCCTATTATTGAATGATAAACTGCCTTCGGGTAGATGCTTTTCAGGATCTCCACAACTTGAA : ::::::::::::::::::::::::::::::::::
Slit 325	Slit 325	Slit 325 33	Slit

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	Kepiacemeni	. rigure Sheet 1	.5 01 39
1470 GGCCATT :	1540 GATTATCTCC :::: -TAAATCTTC	1610 AAAGAATTGG ::: ATTTATATTT	1680 GATTAT
1460 ACCTCTTCG	1530 CTAGCGGAT: ::. CTTTTAZ	1600 CAAACAAAAC :	1670 AGGTACAGAA
1450 GGGACCTTTTCA :::: TTTCA 490	1520 1530 1540  CCAGAACCCCTTTATTTGTGACTGCCATCTCAAGTGGCTAGCGATTATCTCC  :::::  CCTGGAATATTTAAGGGACTTTTAAATCTTC  520	560 1570 1580 1590 1600 1610 ACCAGTGGTGCCCGTGGCCTGGCAAACAAATTGG	1660 AGTATTTCATTCC; :::::::::
1440 CATCGCCAAG	1510 TGTGACTGCC/: :	1580 GCACCAGCCC	1650 GCTAAAGAACAGT : ::: ::: -CGAGAGGAGT
1430 AGCTTCAGAC	1500 CCCTTTATT .:::	1570 GTGCCCGTT	30 1640 ATTCGTTGTTCAGC' :: :::: :TCTTTTGTTCC' 570
1420 CTATATGACAACA:::::::: CTAAATAATAA480	1490 TTTGGCCCAGAAC :::::::: TTAGATCCTGGA- 510	1560 TGAGACCAGTG	1630 AAGAAATTCCG ::::: AGGTATCTT 570
1410 ::::: T-TTCTATTT 470	1480 :::::: CAAACTATGCA	1550 1 ATACCAACCCGATTGAG::: GTA540	1620 1630 1680 1680 1680 1680 1680 1680 1680 168
325	Slit 325	Slit 325	Slit 325

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1750 3GAACCA	1820 AGTTGCG	1890 ACGTAAA	1960 TAAATG
1740 TCGCTGTGAA(	1810 TACACTGCAGA :::: CACTG 640	1880 TTCCTCAATT? :.::: TACCT	1950 AGCATCTGGTG ::::: CTTCGG 680
1730 CTGAAAAGTG	1800 .CATTCCCCAG .: ::.	1870 TTTAAGAAAC 	1940 CATTTGAAGG :. CT
1720 :::: TCAG	1790 TCCCGGAGCA ::: GGAA	1860 CACAGGAATC .:: TGG	20 1930 ATATTGAGGAGGAGCAT .:.::::. TTGTTGGTATGGTTGCT-
1710 CTTTGCGGATCTG : . : . : : : : : : : : : : : : : : : :	1780 CTCAACAAAA :::: CAAA-	1850 TGTTGGAAGC :::::: TTGGGAG- 650	1920 CACAGATATT ::::
1700 GTGGAGACTG	760 TTGCTCTAATCAAAAG :.::.:::: -TACTTAAATCTA	1840 GAATTTACCG' :::	1910 ACAATAAGAT
1690 1700 1710 1720 1730 1740 1750  Slit CGATCAAAATTAAGTGGAGACTGCTTTGCGCTTGCCCTGAAAAGTGTCGCTGTGAAGGAACCA :::::::::::::::::::::::::::::	1760 1770 1780 1790 1800 1810 1820 CAGTAGATTGCTCTAATCAAAATCCCGGAGCACATTCCCCAGTACACTGCAGAGTTGCG : : : : : : : : : : : : : : : : : : :	1830 1840 1850 1860 1870 1880 1890  TCTCAATAATAATGAATTTTACCGTGTTGGAAGCCACAGGAATCTTTAAGAAACTTCCTCAATTACGTAAA  .:::::::::::::::::::::::::::::::::	1900 1910 1920 1930 1940 1950 1960 ATAAACTTTAGCAACATAAAGATCACAGATATTGAGGGGGGGG
Slit 325	Slit 325	Slit 325	slit 325

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2030 GCCTCAA :	2100 TTCTGTG	2170 CATTCTT	2240 AGTGGCT :
2020 3GATTGGAAA	2090 FAGGACTCAG	2160 rgaracrcrc	2230 GCTTGGTTGGGAG; ::::: :: GCTTGTTTGTAT
2010 3ATGTTCAAG	2080 TGACAGTTTCA: ::::: TATCAGAATCA(	2150 CAGGGGCATT	2220 CTACCTGGCT7 :::
2000 TGCAGCATAA(	2080 GTGTGGGGAATGACAGTTTCAT :::::::::::::::::::::::::::::::::	2140 ACAGTTGCAC	2210 ACTGTAACTG0
1990 TTGGAAAATG	050 2060 2070 2080 2090 2100 GCAATCGAATAACCTGTGTGGGGAATGACAGTTTCATAGGACTCAGTTCTGTG :::::::::::::::::::::::::::::::	120 2130 2140 2150 2160 2170 TGATAATCAAATTACTACAGTTGCACCAGGGGCATTTGATACTCTCCATTCTT	190 2200 2210 2220 2230 2240  TTGGCCAATCCTTTTAACTGTAACTGCTACCTGGCTTGGTTGG
1980 ACGAGTAATCGT :::::: GATTTATC	2050 sagaagcaatc	2120 TGTATGATAA	2190 AAACCTCTTGGCC ::::::: -AACATCTTGA 740
1970 1980 2000 2010 2020 2030  Slit AAATACTTCTTACGAGTAATCGTTTGGAAATGTGCAGCATAAGATGTTCAAGGGATTGGAAAGCCTCAA :::::: :::::::::::::::::::::::::::::	2040 201t AACTTTGATGTTGAGAA 325 AAC	2110 2 Slit CGTTTGCTTTCTTTGTA ::::: 325GCTTTC	2180 2 TATCTACTCTAAACCTC ::: :: -:
Slit 325	Slit 325 7	Slit 325	Slit 325

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# **Replacement Figure Sheet 18 of 39**

2310 ACCCATC	: 	2380 CACTTTCTC :. :::: CTTTGTCTC 840	2450 CTTGCC :::::: CTTGCC 890	2520 AAGGAA
2260 2270 2280 2290 2300 2310 CTCACGGGAAATCCTAGAAAACCATACTTCCTGAAAAGAAATACCCATC	::::: GAAGTAC 810	2370 TTGCTCCCCAC :-	2450 GGTTTGAAGGTCTTGCC :::::::::::::::::::::::::::::::::::	2510 CACTGGTTCCC :::
2290 CCATACTICC	:::: :CCTTT	2360 ATGATGACAATAG .:.::::: -AGAAGACTTT	2430 TAGCAACAAG :: CA	2500 AAACCAATTTA :.::: ATACC
2280 SATGTCAAAAA	.:::::. ATCAAATGCCTTT 800	2350  GACGGAAATG	2410 2420 GATACAGTCGTCCGATG' :::::::::::	2490 2 ATCTGGATGGAAACCA ::::::::
2270 GAAATCCTAC	:::: acaaaagtacc 790	2340 CACTTGTGA1	2410 TTGGATACAG . ::::: AATACAG 0	2480 CAGAGTTGTA
2260 ATTGTCACGG	:.::. ATTTAACAA 780	2330 CATTCAGGACTT .:.:::: -TTAAAAGTCTT 820	2400 ATGTACTTGCTTG ::. AGCA 860	2470 AGAGATGTCA
2250 Slit GAGAAAGAAGAATT	::::::::::::::::::::::::::::::::::::::	2320 2330 2340 2350 2360 2370 2380  Slit CAGGATGTGGCCATTCACTTGTGATGACGGAAATGATGACAATAGTTGCTCCCCCACTTTCTC  :::::::::::::::::::::::	2390 2400 2410 2420 2430 2440 2450  GCTGTCCTACTGAATGTACTTGCTTGGATACAGTCGTCCGATGTAGCAACAAGGGTTTGAAGGTCTTGCC:::::::::::::::::::::::::::::::::	2460 2470 2480 2500 2500 2510 2520 Slit GAAAGGTATTCCAAGAGTTGTATCTGGATGGAAACCAATTTACACTGGTTCCCAAGGAA ::::::::::::::::::::::::::::::
Slit	325	Slit 325	Slit 325	Slit 325

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2590 AATCAGA	: ::.: TTTAGTGG 950	2660 CTCCTCG	2730 TGCCTGAA : . : : : : TACCTTAA 1050	2800 ACTGTGATTGTA : ::::. GATAATGAT
2580 ACGCTTTCT	: : TTT 950	2650 AGATGTATTC ::. TAATGA	2720 FTCTGTTGT : : : : FTAATTT 1040	2790 CTTTACTGT :: GA
2570 ACAGAATAAGC	::::::::::::::::::::::::::::::::::::::	2640 265 AACCGTCTGAGATGT ::::::.	2690 2700 2710 2720 2730  TTCGATTACTTTCTCTACATGGAAATGACATTTCTGTTGTGCCTGAA :: .:::::::::::::::::::::::::::::::::	2780 ;AGCCAACCCT(
2560 TTAAGTAACAA	::: ::::::::::::::::::::::::::::::::	2630 TTCTTAGTTAC :::::: ATCTTAA	2700 ACTTTCTCTACATG ::::::::: ACATTCAGTTTG	2770 ATCTAGCAATTGG ::::::
2550 ACTTATAGAC	:: TTAGGA 930	2620 2630 CTCACCTTAATTCTTAG ::::::::::	2690 TTCGATTACTT:::::-::-:-:	2760 CATTATCACAT :::: AATAAT
2540 AACATTTAAC	:: FTCAAGAA 920	2610 TGACCCAGCTC::: TAA	2680 TTAAAGTCTC :::::: TTTAAAT	2750 27 ATCTTTCTGCATTAT:::::::::::::::::::::::::
2530 2540 2550 2560 2570 2580 2590 CTCTCCAACTACAACATTAACACTTATAGACTTAAGACTTAAATCAGA	:::. :: :: :: :: .:: .: .: .: .: .: .: .	2600 2610 2630 2640 2650 2660  Slit GCTTCAGCAACATGACCCTCACCTTAATTCTTAGTTACAACCGTCTGAGATGTATTCCTCCTCG  .:::::::::::::::::::::::::::::::::::	2670 2720 2730 2730 2730 2710 2720 2730 CACCTTTGATGGATTAAAGTCTCTTCGATTACTTTCTCTACATGAAATGACATTTCTGTTGTGCCTGAA :::::::::::::::::::::::::::::::::::	2740 2750 2760 2770 2780 2790 2800 Slit GGTGCTTTCAATGATCTTTATCACATCTAGCAATTGGAGCCAACCCTCTTTACTGTGATTGTA : :::::::::::::::::::::::::::::::::::
Slit	325	slit 325	Slit 325	Slit 325

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		_	
2870 CTGGTCC ::::	2940 2940 GTGGAT	3010 AATAGTG : :	3080 AATTCA ::::: ATTCA 1190
2860 2870 CTCGTTGTGCTGGTCC ::::::	2930 GTCAAGGTCC ::::. GTCAT	3000 GGCACATGTA	3070 GTGATGTCCC
2850 GCCTGGAATTG:::	2920 29 AATTTACCTGTCAA ::::::::	2990 TAAAAATGAT	3060 GGGCAGGACT : 3
TCGGAATATAAGGAGCCT : ::::::::::::::::::::::::::::::::::	2910 CCTCCAAAA	2980 CAAATCCGTG': : :::: C-ATCCAAG	3050 IGGTTTCAAGG :::::
1920   2830   2840   2850   2860   2870     2870     2870     2870     2870     2870     2870     2870     2870     2870     2870     2870     2870	2900 ACTCACAACT0	960 2970 2980 3000 3010 GTGTAACCCCTGCCTATCAAATCCGTGTAAAAATGATGGCACATGTAATAGTG::::::::::	3040 CCTGTCCATA1 :::: TGTC
2820 CCGACTGGG1	2890 TAAACTTTT?	2960 AAGTGTAACC	3030 ACCGATGCAC ::::
2810 2 Slit ACATGCAGTGGTTATCC :::: 325 ACAT	2910 2880 2890 2940 2910 2920 2930 2940 2940 2940 2950 2940 2940 2940 325 TTAATCTGTCATCTGTCTGTGAT 1130	2950 GTCAATATTCTAGCTAA : :::::::-:	3020 3030 3040 3050 3060 3070 3080  Slit ATCCAGTTGACTTTTACCGATGCACCTGTCCATATGGTTTCAAGGGGCCAGGACTGTGATGTCCCAATTCA  ::: :: :: :: :: :: :: ::: ::: ::: :::
Slit ACZ :: 325 ACZ	Slit I 325 I	slit G 325 -	slit A' 325 G'

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3150 TGGATTC	:: :: TGCAAAC 1230	3220 GATAATG :	3290 AGTATAC	3360 TTCAAAG
3100 3110 3120 3130 3140 3150 CCATGTAAACGAGAAGATGGATTCCCACTTAAAGGAAGGA	::.:::::::::::::::::::::::::::::::::::	3210 ATGATTGTGAA	3280 TTGCCCACCTG ::: TTAC	3350 TGCCAGCACGA
3130 TTAAAGGAA	       	3200 TCAACGTIG :	3270 .cacargcctrrgc :: :::::: .cagccarrac 1270	30 3340 AGGACCTGAACCCCT :::::::GTCAGAATCCCC- 1290
3120 AACTTGCCAC	::.::	3190 AATTGTGAAG	3260 TAATAACTACA ::::: CTTCA	3330 GCCCAGGACCT ::: TGTCAG
3110 ACATGGAGG		3180 GAAGGAGAAA	3250 ICGAIGGCAIT ::::: IAGCAI-	3320 GCTGGACTTCTGTGC ::.::::: TCTAAACATCTATT- 1280
3100 ACCCATGTAA	::.:. CAAATT	3170 GATGGATTT	3240 CTACATGTG' .:	3310 GGAGAAGCTO ::
TGCCTG	: :::: TCTTCAGG	3160 3170 3180 3200 3200 3220 Slit TGGTGTATTTGTGATGGATTTGAAGGAGAAATTGTGAAGTCAACGTTGATGATGTGAAGATAATG : :::::::::::::::::::::::::::::::::::	3230 3240 3250 3260 3270 3290 3290 t ACTGTGAAAATAATTCTACATGTCGATGGCATTAATAACTACACATGCCTTTGCCCACCTGAGTATAC ::: 5 ACTGGCTAGCATCTTCAGCCATTAC	3300 3310 3320 3330 3340 3350 3360 Slit AGGTGAGTTGTGAGGACTTCTGTGCCCAGGACCTGCCAGCACCAGCACAAG ::::::::::::::::::::::
Slit	325	Slit 325	Slit 325 12	Slit 325

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	_		
3430 GACATCG	3500 GCTATAC ::: ATAA 1360	3570 3570 3000 3570 3000 3570 3000 3570	3640 AGCCAATATGTC :::::::
3420 TGAACACTGC	3490 3CAGTGAACG	3560 ATGGTCCTCCCT::::::::: ATATTCATCACA	3630 AAATGAGCCAA' ::: 1450
3410 AGGGTACGTAGG' ::::: TTACGTT 1320	0 CCCACTGCACAGAT( : .:: :: -CATCTTCA		590 3630 3640  TGATTGTCAGAATGGAGCTCAGTGTATCGTCAGAATAAATGAGCCAATATGTC :::::::::::::::::::::::::::::::::::
390 3400 TGTGACTGCACACCAG :::::: -GTGGCAGAGCA	3470 AACGGAGCCCA : .	3540 CTGTGAGTTT : :GTAAAA	3610 GAGCTCAGTGTATCGTCAG :::::::::: GCATAAAGTAACCA- 1440
3390 CCAAATGTGAG :::: GTGGG	3460 SAGTGTAAAA ::::: NTTGTGTTA	3530 CAGTGGCTTGTTC : ::: ::: CTTGGGCT-GTT- 1380	3600 TCAGAAIGGA ::: CCIG
3380 CAAAGGGATT	3450 3460 CCAAGACAACAGIGIAAA :.::::::::-: ATTACAAATTGIGITA- 1340 1350	3520 CCGAAGGTTACA :::: :: CCAGAGCI	3590 36 ATTTTGATTGTCAGA :: :: :: ATGATGGCCTG- 1430
3370 3380 3400 3410 3420 3430 Slit TGCATCCTAACTCCAAATGTGACTGCACCAGGGTACGTGGACACTGCGACATCG ::::::::::::::::::::::::::::::::::::	3440 3450 3460 3470 3480 3490 3500 ATTTTGACGACTGCCAAGACAACAAGTGTAAAAACGGAGCCCACTGCACAGATGCAGTGAACGGCTATAC :::::::::::::::::::::::::::::::::	3510 GTGCATATGCC :::: ATGTAT	3580 3 Slit AGCCCCTGTGATAATTT ::::::::::::::::::::::::::::
Slit 325	Slit 325	Slit 325	Slit 325

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3710 AAAGAGTC ::. TGGGAA 1500	3780 3780 346ATGAA 37GGTAA-	0 3850 GGGGCGTGTTC ::::: GCAAATAC 1590	3920 ATGGAAA : :
3690 3700 37 TGTGAATTTTATAAACAAAGAG ::::::::::::::::::::::::::::::::	3770 AGATTGCCACA :::::::	3840 TATCGGGGG: :.: ::	900 GTGGAGACAATCAATG ::::: :::::-:: -TGGAAAAAAAGGTG
3690 AGTGTGAAT1 :::::: TGAGAAC7	3760 FACACTTCA ::.: FTTTTCAAGA	3830 GCGGTAGAACTCTAT ::.:: :::: GCAGTGTTAC-CTGT 1580	3900 AGTGTGGAGA ::::::
3680 AAAATTGGTT? ?	3740 3750 3760 3770 378 TTCGGCCTCAGACGAACATTACACTTCAGATTGCCACCAGATGA :::::::::::::::::::::::::::::::::	3820 GACCATATCGCC ::::	3880 3890 3900 3910  CCAGCTTCTGCCATTTACAGTGTGGAGACAATCAATGAT  : :: :: :: :: :: :: :: :: :: :: :: ::
3660 3670 3680 3690 3700 3710  TCAGGGAGAAAAGTGGATTGGTTAGTGTGAATTTTATAAACAAAGAGTC ::::::::::::::::::::::::::::::::::::	3730 3740 3750 3760 3770 3780  TCAGCCAAGGTTCGGCCTCAGACGAACATAACACTTCAGATTGCCACAGATGAA .: .:.::.::::::::::::::::::::::::::::	3810 3820 3830 38 GTGACAAAGACCATATCGCGGTAGAACTCTATC ::::::::::::::::::::::::::::::	3870 3880 3890 3900 3910 3920 CGGCTCTCATCCAGCTTTTACAGTGTGGAGACAATCAATGGAAA : : : : : : : : : : : : : : : : : :
3660 ATCAGGGAGA.:::::::::::::::::::::::::::::::	3730 TTCAGCCAAG ::: TAC	3800 CTCCTGTATAAGG :::::: -TCCATTA	3870 .ccggcrcrca
3650 Slit AGTGTTTGCCTGGCTA ::: ::: :: 325 AGTCCTCT-	3720 TTATCTTCAGATTCCTTCA :.::::::- CGAATTCCTAC- 1510	3790 3840 3850 GACAGCGGAATCCTCTGTATAAGGGTGACAAAGACCATATCGCGGTAGAACTCTATCGGGGGCGTGTTC :::::::::::::::::::::::::	3860 GTGCCAGCTATGACAC ::: AA-CTTACTA
Slit AGTG ::: 325 AGT- 1460	Slit TTAT 325	Slit GACA	Slit GTGC 325 AA-C

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		-
4060 TGCCAG	4130 CATCCG	4200 CCTGGC
4050 IGTAGGAGGCA	4120 FTCCACGGCTG :: FT	150 4160 4170 4180 4190 4200 GTGAGCTGCAGGACTTCCAGAAGGTGCCGATGCAAACAGGCATTTTGCCTGGC ::::: :::
4040 CTCCACTCTA'	4110 CGGAACCAGC: : ::: TGCTAGC: 1730	4180 CCGATGCAAA( TTTT
4030 SAATTTTGACT .:.:::	4100 CTGGGCAGAA : ::: TTGACATTT	4170 CCAGAAGGTGC ::: GTG-
4020 STCCACTCTG ::::. ACACAP	4090 GCCAGGCCC	4160 GCAGGACTT
4010 TGTCAAAGCA( ::: TGT	4080 GGCATCTCTGC ::::: GGCTT	
4000 Slit ATCATCACTAACT ::::::::::::::::::::::::::	4070 Slit GGAAGAGTAACGT :::: ::: 325 -GAAGTTGAATGA 1700	4140 4 Slit GAACCTTTACATCAACA ::::::: 325TTTTCATC
	4000 4010 4020 4030 4040 4050  TCATCACTAACTTGTCAAAGCAGTCCACTCTGAATTTTGACTCTCCACTCTATGTAGGAGGCATG  :::::::::::::::::::::::::::::::::::	### 4000 ### 4010 ### 4020 #############################

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	Replacemen	t Figure Sheet	23 UI 37
4270 TCACCT	0 CTTGGAAATAA :::::: CAAGGGAAAAT 20	4410 GCCATGGA :::: ATGTA 1870	4480 CACGGGAAGT ::::: CT-AGAAAGT 1910
4260 CAGGCAGGCTTC ::: :: CAGTTTA- 1790	4330 4340 CTTGCCTTGGAAATAA :.::.: CAAGGGAAAT	4400 CTTGGAGGGC	460 4470 4480 GATCAAGTGCAAGCACGGGAAGT :::::::::-:::::::::::::::::::::::::::
4250 4GCCCAGCAGC	4320 3ACCAATGACC	4380 4390 TTCTCCTACAGCTGTAAGTG::::::::::::::::::::	4460 GGCGATCAAGTG ::::: CAAATT 1900
4240 GGCACATGCC?	00 4310 CCTCTGTGACCAACGC : :::::: CATCAGAAAACT	4380 GTTCTCCTACAG :: :: ::: -TTATCAGTCAG 50	4450 TTAACCCATGCCA ::::::::: -TAACACTTCCC- 890
4230 TGTGTGCCCAT:::	4300 GGGCCCCTCT::::	4370 CCATCAATGCGT	4440 GGATCTGTTTA :: TA 1890
4220 ACAAGAAGGTGTG .:: ::: AAAGTTGTT 1780	4290 AAGGATGGATG :::: AAGG	4360 ACCTGCTTGC . : : : : TACAGCTT-~	4430 ATGAAGAGGA ::: TTG
4210 4220 4230 4240 4250 4260 4270 Slit TGTGAGCCATGCCACGAGCCAGCCAGCCAGCCAGCCAGCC	4280 GCGAGTGCCAGG .:.:.:: ACAAAACTA	4350 4360 4410  Slit ATGCGTACATGCCACCTCAATGCGTTCTCCTACAGCTGTAAGTGCTTGGAGGGCCATGGA : :: :: :: :: :: :: :: :: :: :: :: :: :	4420 4430 4440 4450 4460 4470 4480  Slit GGTGTCCTCTGTGAAGAGGAGGATCTGTTTAACCCATGCCAGGCGATCAAGTGCAAGCACGGAAGT  ::::::::::::::::::::::::::::::::
Slit 325	Slit 325	Slit A' : 325 A( 1830	Slit 325

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		replacemen	t rigure sheet	<b>-0 01 0</b> 5
4550 GTGATCG	:.:.: -TAAACA	4620 TTGCCAA ::: TTGA	4690 CCGCTGA : :	4760 AGAAAGT :.: AAA
4540 3GGACAGCT	:::. :. ::.:. GACTTCA-TAAACA 1940	4600 4610 AGCAGCAGGCTATGCTGCTTG ::::::::::::::::::::::::::::::	4680 4 STGCTGTGGACCGC ::::::::::::::::::::::::::::::::	4750 TGGACGAGGTTGAGA :::::::::::::::: TGGACATGATTTAAA 2050
4530 TGGATACACG	:::	4600 AAGCAGCAGGCTAT ::::::::::::::	4670 CAGGAGGGCA(	4740 CCTCCTTTGTGC:::
4520 ATGCAGCAG		4590 TATTACCAA	4660 GTGGGTGTG	4730 TGACGGCTCCTC .:. ::. TCAGTGCCA- 2040
4510 CCTACTGTGA		4580 AGGATAAGAGAT .:.:.:: TGAAATGAG	4650 3AGTGCAGAG	4720 FCGAATGCAC::: FAAGAAACT-
4500 FUTGGGGCAGC	:::::: GGAGCAG 1930	4570 TCGAGGGGAAAGG : .:. -CTGA 1960	4640 TGTCCCGATTA	4710 4720 GGAAATACTCTTTCGAATGCAC :.::.:::.:.::
4550 4530 4540 4550 4540 511 4520 4530 4540 4550 Slit GCAGGCTTTCAGGCCAGCCCCTACTGTGAATGCAGCAGTGGATACACGGGGGGACAGCTGTGATCG	325 CCTGGCTT	4560 4570 4580 4590 4600 4610 4620  Slit AGAAATCTCTTGTCGAGGGAAAGGATAAGAGTTATTACCAAAAGCAGGGCTATGCTGCTTGCCAA  :: :: :: :: :: :: :: :: :: :: :: :: :	4630 4640 4650 4660 4670 4680 4690  Slit ACAACCAAGAAGTGCCAGAGTGCAGGGGTGTGCAGGGGCAGTGCTGTGGACCGCTGA  :::::::::::::::::::::::::::::::::::	4700 4710 4720 4730 4740 4750 4760  Slit GGAGCAAGCGGCGGAAATACTCTTTCGAATGCACTGACGGCTCCTTTTGTGGACGAGGTTGAGAAGT ::::::::::::::::::::::::::

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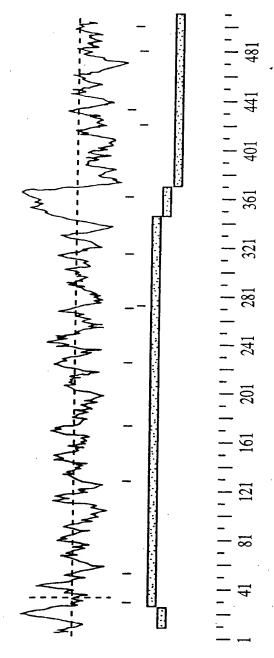
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		_	
4830 AAAAGGTTG :.::: ATATAATTA	4900 TAAAATAC : - : : TTAA		
4820 4830 GTCTTTGGAAAAGGTTG ::: :::.:::	4890 AATATATTGTA ::::::::: AATATGTTTTT 2130		
4810 CGGCAGCTCI	4870 4880 4890 ATAGTGGAAATATTTGAAATATATT::.::::::::::::::::::::::::	4950 :: ::	
0 4800 CCTAAACACACTCC ::: ::: AAACCTC- 2060	4870 CTTCATAGTGC ::: ATATGAGGTT? 2110	4940 ACTTTTTTCTGCA .: :: GCGGCCGC-	Eig. 711 10
4790 TGTGTGTCCT	4860 CTAATGAATG :::::: ATAATGAATT 2100	1920 PATTATGAGAATAAAGAC :.:::::::::::::::::::::::::::::::::::	
4780 GGCTGTACGAGG ::: CTG	4850 CCATGTGGGAC ::: TGGAAATA 2090	910 4920 4930 ACTTATTTATTATGAGAATAAAGACTT' :::::::::::	
4770 4780 4830 4810 4820 4830 Slit GGTGAAGTGCGGGGGGTGTGTCCTAAACACACTCCCGGCAGCTCTGTCTTTGGAAAAGGTTG ::: ::: ::: ::: ::: ::	4840 4850 4860 4870 4880 4890 4900  Slit TATACTTCTTGACCATGTGGACTAATGAATGCTTCATAGTGGAAATATTTGAAATATTGTAAAATAC :::::::::::::::::::::::::::::::	4910 4920 4930 4940 4950 Slit AGAACAGACTTATTTTTTATGAGAATAAAGACTTTTTTCTGCATTTG ::::::::::::::::::::::::::::::::::	
Slit 325	Slit 325	Slit 325	

Applicants: Christopher C. Fraser (as amended)
Serial No.: 09/766,511 Filed: January 19, 2001
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Atty/Agent: Mario Cloutier
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	Kep	nacement	rigure	Sneet 29	of 39
GQVAWARV 70	 	PAGSFQAR 140	20 AVTSEFHL	::::::: AVTSEFHL 210	90 EGQPPPSY ::::::: EGQPPPSY 280
'YRGDSGEQV 60	1	EYECRVSTF 130	10 -KGTTSSRSFKHSRSAAVTSEFHL	::::::::::::::::::::::::::::::::::::::	80 EGAMLKCLS: ::::::: EGAMLKCLS! 270
7LGQDAKLPCF 50	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	LRNAVQADEG 120	KGTTSS	::::: DTEVKGTTSS 190	70 EDQNLWHIGR ::::::::: EDQNLWHIGR 260
LLLLLLASFTGRCPAGELETSDVVTVVLGQDAKLPCFYRGDSGEQVGQVAWARV 20 30 40 50 60 70	1	LHVSPAYEGRVEQPPPRNPLDGSVLLRNAVQADEGEYECRVSTFPAGSFQAR 90 130 110 120		ALEEGQGLTLAASCTAEGSPAPSVTWDTEVKGTTSSRSFKHSRSAAVTSEFHL 160 170 180 190 200	50 60 70 80 90  PGLLQDQRITHILHVSFLAEASVRGLEDQNLWHIGREGAMLKCLSEGQPPP ::::::::::::::::::::::::::::::::::
ASFTGRCPAGI 30	; ; ; ; ;	AYEGRVEQPPE 100	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	GLTLAASCTA 170	50 )QRITHILHVS :::::::::
AWLLLLLLL 20	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	SKYGLHVSP <i>i</i> 90		NPGPALEEGÇ 160	40 VVSHPGLLQD ::::::::: VVSHPGLLQD 230
T364 MPLSLGAEMWGPEAWLL 10		DAGEGAQELALLHSKYG 80	1 1 1 1 1 1 1 1	LRLRVLVPPLPSLNPGP 150	30 40 50 70 90  ALT VPSRSMNGQPLTCVVSHPGLLQDQRITHILHVSFLAEASVRGLEDQNLWHIGREGAMLKCLSEGQPPPSY ::::::::::::::::::::::::::::::::::
T364	ALT	T364	ALT	T364	ALT T364

Fig. 3E

Applicants: Christopher C. Fraser (as amended) Serial No.: 09/766,511 Filed Filed: January 19, 2001 Title: Nucleic acids encoding Tango 405 and functional fragments and

uses thereof (as amended)

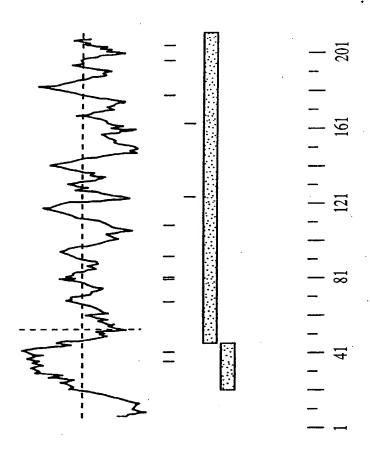
Atty/Agent: Mario Cloutier Attorney Docket No.: MPI00-537OMNIRCEM

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		_							
100 110 120 130 140 150 160 ALT NWTRLDGPLPSGVRVDGDTLGFPPLTTEHSGIYVCHVSNEFSSRDSQVTVDVLADPQEDSGKQVDLVSAS	::::::::::::::::::::::::::::::::::::::	; ; ; ;	::::::::::::::::::::::::::::::::::::::	230 240 250 260 270 - SEEPEGRSYSTLTTVREIETQTELLSPGSGRAEEEEDQDEGIKQAMNHFVQEN	T364 AEGHPDSLKDNSSCSVMSEEPEGRSYSTLTTVREIETQTELLSPGSGRAEEEEDQDEGIKQAMNHFVQEN				
150 ADPQEDSG	:::::: -DPQEDSG] 340	220 ISHHTDPRS	SHHTDPRS	270 DQDEGIKQA	::::::::::::::::::::::::::::::::::::::	480			
140 DSQVTVDVI	::::::: DSQVTVDVI 330	210 RENSIRRLE	::::::: RENSIRRLE 400	260 GSGRAEEEF	::::::: GSGRAEEE	470			
130 CHVSNEFSSR	::::::::::::::::::::::::::::::::::::::	170 180 190 200 210 220 ALT VVVVGVIAALLFCLLVVVVVLMSRYHRRKAQQMTQKYEEELTLTRENSIRRLHSHHTDPRSQ	::::::::::::::::::::::::::::::::::::::	250 ETQTELLSP	::::::::::::::::::::::::::::::::::::::	460			
0 TEHSGIYVC	::::::: TEHSGIYVC 310	0 RRKAQQMTQ	::::::: RRKAQQMTQ 380	240 STLTTVREI	::::::: STLTTVREI	450			
120 TLGFPPLTT	::::::: ;DTLGFPPLT' 300	190 WVLMSRYHRI	::::::: VVLMSRYH 370	230 SEPEGRSY	:::::::	440	HLV	••	HLV 510
110 PSGVRVDGD	::::::: PSGVRVDGD 3	180 LLFCLLVVV	::::::: ALLFCLLVVV 360	0)	: ONSSCSVMS	430	ZSO ALT GTLRAKPTGNGIYINGRGHLV	••	GTLRAKPTGNGIYINGRGHLV 0 500 510
100 WTRLDGPL1	::::::::::::::::::::::::::::::::::::::	170 VVVGVIAA	::::::::::::::::::::::::::::::::::::::	1 1 1	EGHPDSLKI	4,	TLRAKPTGI		TLRAKPTGI 5(
ALT N	: T364 N	ALT V	: T364 V 350	ALT -	T364 A	420 60 60 60	ALT G		T364 G

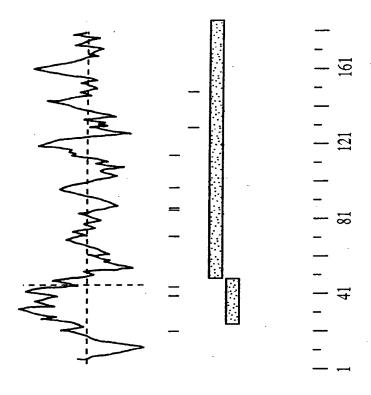
Applicants: Christopher C. Fraser (as amended)
Serial No.: 09/766,511 Filed: January 19, 2001
Title: Nucleic acids encoding Tango 405 and functional fragments and uses thereof (as amended)
Atty/Agent: Mario Cloutier
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				, Jan		1011	it I I	Sui	CS	116	ci.	33	OI .	39		
70	CFSEG	CFSEG			FSYFL	••	LSYFL			MNKIY	•	KSGVF				
09	SIRIWSVAGISIALLSACFIVSCVVTYHFTYGETGKRLSELHSYHSSLTCFSEG	TIRIWSAAVISMLILSTCFIASCVVTYQFIMDQPSRRLYELHTYHSSLTCFSEG	09	130	ONFIVOOLNES		SFGSSCYLISTKENFWSTSEQNCVQMGAHLVVINTEAEQNFITQQLNESLSYFL 90 130	) ) !	200	ICETRRNSICE	•	TPMNPIFQKSGVF	170			
50	TYGETGKRL	TIMDOPSRRL	20	120	HLVVFNTEAE	•••	ILVVINTEAE( 120	)   	190	(PTGWGWNDV	••	(MSGSG	20			
40	IVSCVVTYHE	IASCVUTYQE	40	110	EQNCVEMGAE	•••••••••••••••••••••••••••••••••••••••	EQNCVQMGAF 110		180	EQCASIVEWE	••	GNGSMILLSVKMSGSG-	160			
30	ISIALLSACE	ISMLLLSTCE	30	100	SSEEKVWSKS	•••	STKENFWSTS 100		170	WHLGEPNHSA	•	GNGS	150			
20	WLSLRLWSVAG		20	06	WKSFGSSCYFI		WKSFGSSCYLI 90		160	DKTPYEKNVRF						
10	human MMQEQQPQSTEKRGWL	murine MVQERQSQGKGVC-W-	10	80	human TKVPAWGCCPASWKSFGSSCYFISSEEKVWSKSEQNCVEMGAHLVVFNTEAEQNFIVQQLNESFSYFL		murine TMVSEKMWGCCPNHWK 70 80		150	human GLSDPQGNNNWQWIDKTPYEKNVRFWHLGEPNHSAEQCASIVFWKPTGWGWNDVICETRRNSICEMNKIY		murine GLSDPKVMAN				
	human M	murine M <sup>7</sup>			human Tl	••	murine TM		140	human Gl	••	murine G1	140		hiiman I.	

Fig. 4(

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		1	igure sheet 34 (	1 39
70 TGTGG	.: : AGCTG 0	140 ACATA : ATTAT 0	210 AAGGG ::::: AAGGG	CTACT:::
60 SACTCTGGTC	::::::::::::::::::::::::::::::::::::::	110 120 130 TTCATTGTGAGCTGTAGTAACTTACCATTTTA ::::::::::::::::::::::::::::::::	160 170 180 190 200 210 210  AGGCTGTCTGAACTACATATCATTCAAGTCTCACCTGCTTCAGTGAAGGG ::.::::::::::::::::::::::::::::::	230 240 250 260 270  TGGGGATGTTGCCCAGCTTCTTGGAAGTCATTTGGTTCCAGTTGCTACT ::::::::::::::::::::::::::::::::::
50 GTCCCTGA(	GACCCTGAG	120 GTAGTAACT' ::.::: GTGGTGACT'	190 GTCTCACCT::::: GTCTCACCT	250 260 TGGAAGTCATTTGG :::::::::: TGGAAGTCATTTGG
40 AGGCTGGTT	: ::: GTCTGCTG 40	O TGAĞCTGT :::::: CGAĞCTGT	0 TCATTCAA :::::: CCATTCCA(	250 TCTTGGAA( ::::: CACTGGAA(
4 SAGAAAAGA	.:::: GGAAGGGA 30	110 SCTTCATTGT ::::::: STTTCATTGC	180 CACTCATATO ::::::: CACACATACO	240 TGCCCAGCT: ::::::: TGCCCAAATC
30 AAAGTACAG	: :	90 100 ACTCCTCAGTGCTTGC ::::::::::	170  CTGAACTA  ::::::  RTGAACTT	230 TGGGGATGTT ::::::: TGGGGATGCT 230
20 GCAACCTC	.:::: ACAATCCC/ 20	90 GCACTCCT( ::::: TTACTCTT(	160 AAAAGGCTG: :::::: AGAAGACTA: 150	
10 20 40 50 50 human ATGATGCAAGCAACCTCAAAGTACAGAGAAAAAGAGGCTGGTTGTCCCTGAGACTCTGGTCTGTGTGG	::::::::::::::::::::::::::::::::::::::	80 CTGGGATTTCCATT ::::::::: CTGTGATTTCCATG	150 160 200 210  human TGGTGAAACTGGCAAAAGGCTGTCTGAACTACACTCATTCAAGTCTCACCTGCTTCAGTGAAGGG  : : : : : : : : : : : : : : : : : :	220 240 250 270 human ACAAAGGTGCCAGCC————TGGGGATGTTGCCCAGCTTCTTGGAAGTCATTTGGTTCCAGTTGCTACT ::::::::::::::::::::::::::::::::::
human	murine	human murine	human murine	human murine

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Atty/Agent: Mario Cloutier Attorney Docket No.: MPI00-537OMNIRCEM

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340 3ATTTGGT	ATCTGGT	410 ITTTTCTG :::: ICTTCCTG 410	480 AAAATGTCA ::::::: AAAATGTCA 480	550 AACCTAC						
330 AGATGGGAGCAC	::::::::::::::::::::::::::::::::::::::	400 GTCATTTTCTT? :::: ::::: GTCACTTTCTT? 400	470 CCTTATGAGAAA ::::::: CCTTTCAGTCAA	540 TAGTCTTCTGGA						
340 330 340 340 340 330 340 340 340 340	::::::::::::::::::::::::::::::::::::::	350 360 370 380 390 400 410  TGTGTTCAACACAGAAGCAGAATTTCATTGTCCAGCAGCTGAATGAGTCATTTTCTTATTTTCTG ::::::::::::::::::::::::::::::::	420 430 440 450 460 470 480  GGGCTTTCAGACCCACAAGGTAATAATTGGCAATGGATTGATAAGACACCTTATGAGAAAATGTCA ::::::::::::::::::::::::::::::::::::	490 500 510 520 530 540 550 human GATTTTGGCACCTAGGTGAGCCAATCATTCTGCAGAGCAATGTGCTTCAATAGTCTTCTGGAAACCTAC :::::::::::::::::::::::::::::::						
310 FAAGAGTGAGC	: ::::: CACCAGTGAGC/ 310	380 TTCATTGTCCAG :::: :::: TTCATCACCCAG	450 ATTGGCAATGG2 ::::::: AATGGCAATGG2 450	510 520 53  TGAGCCCAATCATTCTGCAGAGCAATGTG :::::::::::::::::::::::::::::::::						
300 GTTTGGTC	: :::. TTCTGGAGG 300	370 ;AGCAGAAT; :::::::;	440 TAATAATAI: :::::::::	510 ::::::::::::::::::::::::::::::::::::						
290 TGAAGAGAAG	.:.::: :caaggagaac 290	360 ACAGAAGCAG ::::::::	0 TTCAGACCCACAAGG ::::::::::::: TTCGGATCC-CAAGG	500 .cctaggrgag :: .::. .ccccargaa						
280 human TCATTTCCAGTGAAGA	::::::: TCATTTCTAC 280	350 TGTGTTCAACACAGAA ::::::::::: GGTGATCAATACTGAA 350	420 GGGCTTTCAG ::::::: GGTCTTTCGG 420	490 GATTTTGGCACC :.:: ::::: GGTTCTGGCACC 490						
human	murine	human murine	human murine	human murine						

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human CTA

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M.T.	••	TM 70	140 LGL	::: LGL 140		OI	ᆸ	
		Dectin MVQERQSQGKGVCWTLRLWSAAVISMLLLSTCFIASCVVTYQFIMDQPSRRLYELHTYHSSLTCFSEGTM 10 20 30 40 50 50	80 90 100 110 120 140 mT405 VSEKMWGCCPNHWKSFGSSCYLISTKENFWSTSEQNCVQMGAHLVVINTEAEQNFITQQLNESLSYFLGL	::::::::::::::::::::::::::::::::::::::		QKSGVFQ	:::: .: .: .: .: .: .: .: .: .: .: .:	
RLWOAAVIOMLLLUOICFIAOCVVIIQFIMUQPORKLIELHIIHOSLICFOEGIM		FIMDQPSRRLYE 50	120 HLVVINTEAEQN	::::::::::::::::::::::::::::::::::::::	170	-II	.: NPSKWGWNDVFC 190	
FIASCVVIIQ	•••	FIASCVVTYQ 40	110 SEQNCVQMGA	:::::::: SEQNCVQMGA 110		!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!	EERCVSIVYW 180	Fig. 4G
		VISMLLLSTC 30	100 ISTKENFWST	::::::::::::::::::::::::::::::::::::::	0:	MSGSGTPMNP	. : : EWHPHEPNLP 170	
		/CWTLRLWSAA 20	90 HWKSFGSSCYI	::::::::::::::::::::::::::::::::::::::	150 160	SNGSMILLSVK	:. [DDTPFSQNVR] 160	
	TIMONORPÄRÄRÄRÄRA COFIU	MVQERQSQGKGV 10	80 VSEKMWGCCPNF			mT405 SDPKVMANGNGSMILLSVKMSGSGTPMNP-	:::. SDPQGNGKWQWI	
7 C L E	MT.403	Dectin	mT405	Dectin		mT405	Dectin	

uses thereof (as amended)

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••	LTCFSE	70	140	ESFSYF	•••	ESLSYF	140		CEMNKI	•••	CEMKKI	-	
	STHTYHES	09	130	NFIVQQLN	•••	NFITQQLN	130	200	CETRRNSI	•••	CDSKHNSI	200	
	TLRLWSAAVISMLLLSTCFIASCVVTYQFIMDQPSRRLYELHTYHSSLTCFSEG	20	120	/FNTEAEQI		/INTEAEO	120	190	SWGWNDVI		KWGWNDVF	190	
•	TYQFIMI		<del></del>	MGAHLVV	•••	MGAHLVV	П	П	VEWKPIG	•••	VYWNPSK	7	
	:::::	40	110	EQNCVE		EQNCVQI	110	180	EQCASI		ERCVSI	180	Fig. 4H
*****	. :::::	30	100	<b>EEKVWSKS</b>	::	KENFWSTS	100	170	GEPNHSA		HEPNLPE	170	Fig
•	SAAVISN		, ,	CYFISSE	•	CYLISTE	` '		NVRFWHI	•••	NVRFWHI	` '	
	-::: -TLRLW	20	90	IKSFGSS(	•••	1KSFGSS(	06	160	KTPYEKI	•	DTPFSQ	160	
t	: ::::::::::::::::::::::::::::::::::::	10	80	hT405 TKVPAWGCCPASWKSFGSSCYFISSEEKVWSKSEQNCVEMGAHLVVFNTEAEQNFIVQQLNESFSYFL	•••••••••••••••••••••••••••••••••••••••	Dectin TMVSEKMWGCCPNHWKSFGSSCYLISTKENFWSTSEQNCVQMGAHLVVINTEAEQNFITQQLNESLSYFL	80	150	hT405 GLSDPQGNNNWQWIDKTPYEKNVRFWHLGEPNHSAEQCASIVFWKPTGWGWNDVICETRRNSICEMNKIYL	•••	GLSDPQGNGKWQWIDDTPFSQNVRFWHPHEPNLPEERCVSIVYWNPSKWGWNDVFCDSKHNSICEMKKIYL	150	
	 MVQERQSQG			TKVPA	:	TMVSEK			GISDPQ	•••			
NI405 MMQEQQPQSTEKKGWLSLKLWSVAGISIALLSACFIVSCVVTYHFTYGETGKRLSELHSYHSSLTCFSEG	Dectin			hT405		Dectin			hT405		Dectin		

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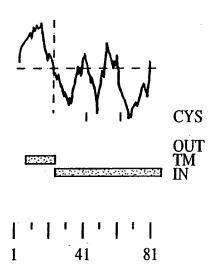


Fig. 5A